# WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Tuesday, November 09, 2004

| Hide? | Set Name | Query | Hit Count |
|---|---|---|---|
| | | *DB=USPT; PLUR=YES; OP=AND* | |
| ☐ | L1 | glycosyltransferase or glycosyl-transferase | 949 |
| ☐ | L2 | L1 same sucrose | 39 |
| ☐ | L3 | L1 same sucros$ | 40 |
| ☐ | L4 | L1.clm. and method.clm. and (inhibitor or inactivator or inhibition or regulator or modulator or modulates or antagonists or antagonize or antagonise or blocker or blocks or blocked).clm. | 2 |
| ☐ | L5 | L1 near25 (inhibitor or inactivator or inhibition or regulator or modulator or modulates or antagonists or antagonize or antagonise or blocker or blocks or blocked).clm. | 1 |
| | | *DB=EPAB,JPAB,DWPI; PLUR=YES; OP=AND* | |
| ☐ | L6 | glycosyltransferase or glycosyl-transferase | 416 |
| ☐ | L7 | L6 near25 (inhibitor or inactivator or inhibition or regulator or modulator or modulates or antagonists or antagonize or antagonise or blocker or blocks or blocked).clm. | 0 |

END OF SEARCH HISTORY

```
### Status: Signed Off. (1 minutes)

### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009998...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 04.16.00D

Last logoff:  06oct04 11:13:23
Logon file405 06oct04 14:21:51
* * *
SYSTEM:HOME
Cost is in DialUnits
Menu System II: D2 version 1.7.9 term=ASCII
                     *** DIALOG HOMEBASE(SM) Main Menu ***

 Information:
  1.  Announcements (new files, reloads, etc.)
  2.  Database, Rates, & Command Descriptions
  3.  Help in Choosing Databases for Your Topic
  4.  Customer Services (telephone assistance, training, seminars, etc.)
  5.  Product Descriptions

 Connections:
  6.  DIALOG(R) Document Delivery
  7.  Data Star(R)

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      /H = Help            /L = Logoff          /NOMENU = Command Mode


Enter an option number to view information or to connect to an online
 service.  Enter a BEGIN command plus a file number to search a database
(e.g., B1 for ERIC).
?b 155

      06oct04 14:21:52 User228206 Session D2253.1
           $0.00    0.200 DialUnits FileHomeBase
     $0.00  Estimated cost FileHomeBase
     $0.00  Estimated cost this search
     $0.00  Estimated total session cost   0.200 DialUnits


File 155:MEDLINE(R) 1951-2004/Oct W1
       (c) format only 2004 The Dialog Corp.
*File 155: Medline has been reloaded. Accession numbers
have changed. Please see HELP NEWS 154 for details.

      Set  Items  Description
      ---  -----  -----------
?e quorum sensing

Ref   Items  Index-term
E1       14  QUOROM
```

```
E2      851  QUORUM
E3        0 *QUORUM SENSING
E4        1  QUORUMQUENCHING
E5        2  QUORUMS
E6        1  QUORUMSENSING
E7        1  QUOSO
E8        3  QUOT
E9      823  QUOTA
E10      10  QUOTABLE
E11       1  QUOTACP
E12       3  QUOTANE

          Enter P or PAGE for more
?s e6
      S1        1  'QUORUMSENSING'
?s quor? (3n) sens?
             882  QUOR?
          832533  SENS?
      S2      780  QUOR? (3N) SENS?
?e autoinducer

Ref   Items  Index-term
E1       11  AUTOINDUCE
E2       26  AUTOINDUCED
E3      302 *AUTOINDUCER
E4      106  AUTOINDUCERS
E5        6  AUTOINDUCES
E6       17  AUTOINDUCIBLE
E7        1  AUTOINDUCIBLY
E8        2  AUTOINDUCIDA
E9        1  AUTOINDUCIDO
E10      28  AUTOINDUCING
E11       1  AUTOINDUCTIBILITY
E12     341  AUTOINDUCTION

          Enter P or PAGE for more
?s autoinduc?
      S3      748  AUTOINDUC?
?ds

Set     Items   Description
S1          1   'QUORUMSENSING'
S2        780   QUOR? (3N) SENS?
S3        748   AUTOINDUC?
?s s1 or s2 or s3
               1  S1
             780  S2
             748  S3
      S4    1310  S1 OR S2 OR S3
?e succrose

Ref   Items  Index-term
E1        1  SUCCR
E2        1  SUCCRALFAT
E3        7 *SUCCROSE
E4        2  SUCCS
E5        1  SUCCSES
E6        1  SUCCSSFULLY
E7        1  SUCCTION
E8        1  SUCCUBANCE
E9        2  SUCCUBANZA
E10       1  SUCCUBANZE
E11       1  SUCCUBI
E12       1  SUCCUDANEOUS

          Enter P or PAGE for more
?s e3
```

```
      S5       7  'SUCCROSE'
?s sucrose
      S6   41264  SUCROSE
?e sucrose

Ref    Items    RT  Index-term
E1         4        SUCROS
E2         2        SUCROSA
E3     41264     6 *SUCROSE
E4        13        SUCROSE - FRUCTAN 6-FRUCTOSYLTRANSFERASE
E5      1390        SUCROSE --ADMINISTRATION AND DOSAGE --AD
E6       665        SUCROSE --ADVERSE EFFECTS --AE
E7       469        SUCROSE --ANALOGS AND DERIVATIVES --AA
E8       475        SUCROSE --ANALYSIS --AN
E9        35        SUCROSE --ANTAGONISTS AND INHIBITORS --AI
E10       52        SUCROSE --BIOSYNTHESIS --BI
E11      113        SUCROSE --BLOOD --BL
E12       23        SUCROSE --CEREBROSPINAL FLUID --CF

          Enter P or PAGE for more
?s sucrose?
      S7   41279  SUCROSE?
?ds

Set     Items   Description
S1          1   'QUORUMSENSING'
S2        780   QUOR? (3N) SENS?
S3        748   AUTOINDUC?
S4       1310   S1 OR S2 OR S3
S5          7   'SUCCROSE'
S6      41264   SUCROSE
S7      41279   SUCROSE?
?s s4 (25n) (s5 or s6 or s7)
            1310  S4
               7  S5
           41264  S6
           41279  S7
      S8       0  S4 (25N) (S5 OR S6 OR S7)
?s s4 and (s5 or s6 or s7)
            1310  S4
               7  S5
           41264  S6
           41279  S7
      S9       1  S4 AND (S5 OR S6 OR S7)
?t s9/9/all
```

**9/9/1**

DIALOG(R)File 155:MEDLINE(R)


16188354  PMID: 15090509

**LuxS-mediated signaling in Streptococcus mutans is involved in regulation of acid and oxidative stress tolerance and biofilm formation.**

Wen Zezhang T; Burne Robert A
Department of Oral Biology, College of Dentistry, University of Florida, Gainesville, FL 32610, USA.

Journal of bacteriology (United States) May 2004, 186 (9) p2682-91, ISSN 0021-9193 Journal Code: 2985120R
Contract/Grant No.: DE 12236; DE; NIDCR; DE 13239; DE; NIDCR; DE 15501; DE; NIDCR
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

LuxS-mediated **quorum sensing** has recently been shown to regulate important physiologic functions and virulence in a variety of bacteria. In

this study, the role of luxS of Streptococcus mutans in the regulation of traits crucial to pathogenesis was investigated. Reporter gene fusions showed that inactivation of luxS resulted in a down-regulation of fructanase, a demonstrated virulence determinant, by more than 50%. The LuxS-deficient strain (TW26) showed increased sensitivity to acid killing but could still undergo acid adaptation. Northern hybridization revealed that the expression of RecA, SmnA (AP endonuclease), and Nth (endonuclease) were down-regulated in TW26, especially in early-exponential-phase cells. Other down-regulated genes included ffh (a signal recognition particle subunit) and brpA (biofilm regulatory protein A). Interestingly, the luxS mutant showed an increase in survival rate in the presence of hydrogen peroxide (58.8 mM). The luxS mutant formed less biofilm on hydroxylapatite disks, especially when grown in biofilm medium with **sucrose** , and the mutant biofilms appeared loose and hive-like, whereas the biofilms of the wild type were smooth and confluent. The mutant phenotypes were complemented by exposure to supernatants from wild-type cultures. Two loci, smu486 and smu487, were identified and predicted to encode a histidine kinase and a response regulator. The phenotypes of the smu486 smu487 mutant were, in almost all cases, similar to those of the luxS mutant, although our results suggest that this is not due to AI-2 signal transduction via Smu486 and Smu487. This study demonstrates that luxS-dependent signaling plays critical roles in modulating key virulence properties of S. mutans.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--physiology--PH; *Biofilms--growth and development--GD; *Oxidative Stress; *Signal Transduction; *Streptococcus mutans--physiology--PH; Hydrogen-Ion Concentration; Regulon; Virulence --genetics--GE

CAS Registry No.: 0 (Bacterial Proteins); 0 (LuxS protein, Bacteria)

Record Date Created: 20040419

Record Date Completed: 20040520

?logoff hold

06oct04 14:23:47 User228206 Session D2253.2
$5.14 1.607 DialUnits File155
$0.21 1 Type(s) in Format 9
$0.21 1 Types
$5.35 Estimated cost File155
$0.50 TELNET
$5.85 Estimated cost this search
$5.85 Estimated total session cost 1.807 DialUnits

### Status: Signed Off. (2 minutes)

### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009998...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
********
ENTER PASSWORD:
******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected

Dialog level 04.16.00D

Reconnected in file 155 06oct04 14:24:43
* * *

File 155:MEDLINE(R) 1951-2004/Oct W1
(c) format only 2004 The Dialog Corp.

*File 155: Medline has been reloaded. Accession numbers
have changed. Please see HELP NEWS 154 for details.

```
      Set  Items  Description
      ---  -----  -----------
Cost is in DialUnits
?ds

Set     Items   Description
S1          1   'QUORUMSENSING'
S2        780   QUOR? (3N) SENS?
S3        748   AUTOINDUC?
S4       1310   S1 OR S2 OR S3
S5          7   'SUCCROSE'
S6      41264   SUCROSE
S7      41279   SUCROSE?
S8          0   S4 (25N) (S5 OR S6 OR S7)
S9          1   S4 AND (S5 OR S6 OR S7)
?s mutans? (25n) sucros?
            5898  MUTANS?
           41283  SUCROS?
     S10     697  MUTANS? (25N) SUCROS?
?s s10 and (capsul? or media or medium?)
             697  S10
           50357  CAPSUL?
          210895  MEDIA
          205746  MEDIUM?
     S11     123  S10 AND (CAPSUL? OR MEDIA OR MEDIUM?)
?s s11/2000:2004
             123  S11
         2510633  PY=2000 : PY=2004
     S12      28  S11/2000:2004
?s s11 not s12
             123  S11
              28  S12
     S13      95  S11 NOT S12
?target s13/all
Your TARGET search request will retrieve up to 50 of the statistically most
relevant records.
Searching ALL records
...Processing Complete
     S14      50  TARGET - S13
Ending TARGET search. Enter TARGET to do another search in the present
file(s), or BEGIN new file(s).  Enter LOGOFF to disconnect from Dialog
?t s14/9/all
```

**14/9/1**



08367460   PMID: 2532001

**The influence of Streptococcus mutans on adhesion of Candida albicans to acrylic surfaces in vitro.**

Branting C; Sund M L; Linder L E

Department of Oral Microbiology, Huddinge University Hospital, Karolinska Institute, Sweden.

Archives of oral biology (ENGLAND) 1989, 34 (5) p347-53, ISSN 0003-9969 Journal Code: 0116711

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: DENTAL; INDEX MEDICUS

Adhesion of Candida albicans and Streptococcus mutans was studied by incubation of radiolabelled cells with acrylic test specimens in a chemically defined growth medium. Strep. mutans adhered firmly in the presence of **sucrose** , while C. albicans was only loosely attached to the

# NiceProt View of TrEMBL: Q99QI5

Printer-friendly view | Request update | Quick BlastP search

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

*Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.*

**Entry information**

| | |
|---|---|
| Entry name | **Q99QI5** |
| Primary accession number | **Q99QI5** |
| Secondary accession number | Q7CE98 |
| Entered in TrEMBL in | Release 17, June 2001 |
| Sequence was last modified in | Release 17, June 2001 |
| Annotations were last modified in | Release 28, October 2004 |

**Name and origin of the protein**

| | |
|---|---|
| Protein name | **Competence stimulating protein** |
| Synonym | **Competence stimulating peptide,** |
| Gene name | **Name: comC**<br>OrderedLocusNames: SMU.1915 |
| From | Streptococcus mutans [TaxID: 1309] |
| Taxonomy | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus. |

**References**

[1] SEQUENCE FROM NUCLEIC ACID.
**STRAIN**=GB14, H7, LT11, NG8, and UA159;
DOI=10.1128/JB.183.3.897-908.2001;MEDLINE=21142515;PubMed=11208787 [NCBI, ExPASy, EBI, Israel, Japan]
Li Y.H., Lau P.C.Y., Lee J.H., Ellen R.P., Cvitkovitch D.G.;
"Natural genetic transformation of Streptococcus mutans growing in biofilms.";
J. Bacteriol. 183:897-908(2001).

[2] SEQUENCE FROM NUCLEIC ACID.
**STRAIN**=UA159 / ATCC 700610 / Serotype c;
DOI=10.1073/pnas.172501299;MEDLINE=22295063;PubMed=12397186 [NCBI, ExPASy, EBI, Israel, Japan]
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P., Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen.";
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

**Comments**

None

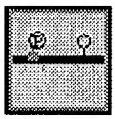
**Cross-references**

| | |
|---|---|
| EMBL | AF277152; AAK01542.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF277153; AAK01543.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF277155; AAK01545.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF277156; AAK01546.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF277157; AAK01547.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]<br>AE015016; AAN59526.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] |
| CMR | Q99QI5; SMU.1915. |
| ProDom | [Domain structure / List of seq. sharing at least 1 domain] |
| HOBACGEN | [Family / Alignment / Tree] |
| ProtoMap | Q99QI5. |
| PRESAGE | Q99QI5. |
| ModBase | Q99QI5. |
| SMR | Q99QI5; 38FA62B6F78FC3BF. |
| SWISS-2DPAGE | Get region on 2D PAGE. |
| UniRef | View cluster of proteins with at least 50% / 90% identity. |

**Keywords**

**Complete proteome**.

**Features**



Feature table viewer

| Key | From | To | Length | Description |
|---|---|---|---|---|
| CHAIN | 26 | 46 | 21 | competence stimulating protein. |

**Sequence information**

Length: **46 AA** [This is the length of the unprocessed precursor]

Molecular weight: **5211 Da** [This is the MW of the unprocessed precursor]

CRC64: **38FA62B6F78FC3BF** [This is a checksum on the sequence]

```
         10         20         30         40
          |          |          |          |
MKKTLSLKND FKEIKTDELE IIIGGSGSLS TFFRLFNRSF TQALGK
```

Q99QI5 in FASTA format

*View entry in original TrEMBL format*
*View entry in raw text format (no links)*
*Request for annotation of this TrEMBL entry*

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

==========

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query length: 21 AA
Date run: 2004-11-09 12:04:31 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,621,919 sequences; 518,174,383 total letters

Taxonomic view | NiceBlast view | Printable view

**List of potentially matching sequences**

Send selected sequences to Clustal W (multiple alignment) Submit Query
Select up to...

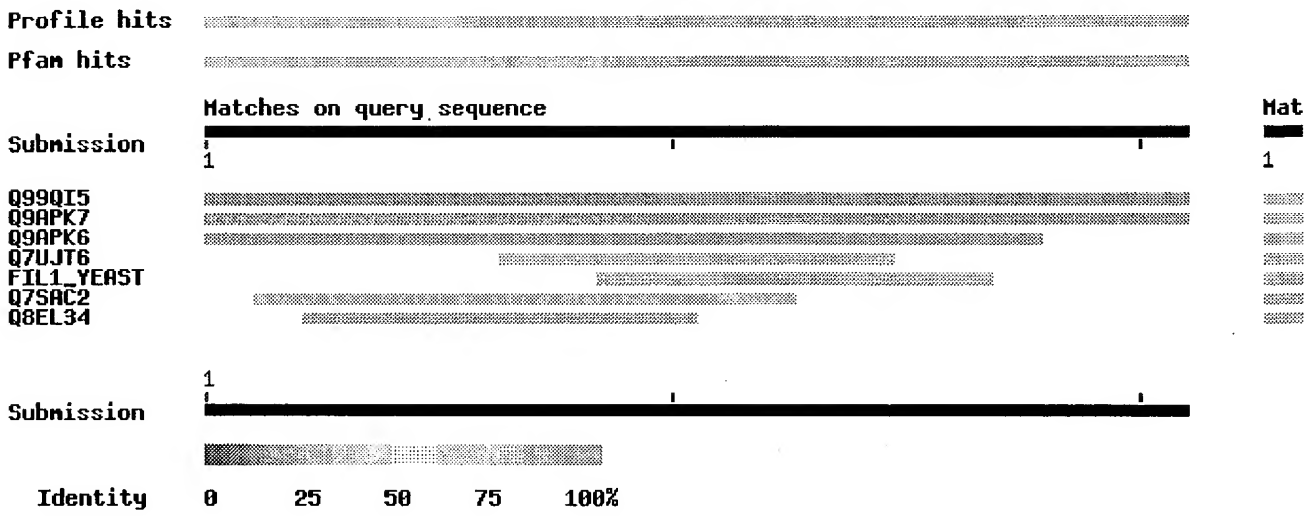
☐ Include query sequence

| | Db | AC | Description | Score | E-value |
|---|---|---|---|---|---|
| ☐ | tr | Q99QI5 | Competence stimulating protein (Competence stimulating... | 68 | 2e-11 |
| ☐ | tr | Q9APK7 | Competence stimulating protein [comC] [Streptococcus m... | 68 | 2e-11 |
| ☐ | tr | Q9APK6 | Competence stimulating protein [comC] [Streptococcus m... | 57 | 4e-08 |
| ☐ | tr | Q7UJT6 | Acriflavine resistance protein B [acrB] [Rhodopirellul... | 32 | 1.4 |
| ☐ | sp | P38771 | FIL1_YEAST FIL1 protein, mitochondrial precursor [FIL1... | 30 | 4.5 |
| ☐ | tr | Q7SAC2 | Predicted protein [NCU06309.1] [Neurospora crassa] | 30 | 4.5 |
| ☐ | tr | Q8EL34 | Hypothetical conserved protein [OB3397] [Oceanobacillu... | 29 | 8.0 |

**Graphical overview of the alignments**

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(Help) (use ScanProsite for more details about PROSITE matches)




**Alignments**

tr Q99QI5 **Competence stimulating protein (Competence stimulating peptide,) [comC] [Streptococcus mutans]** 46 AA align

Score = 67.7 bits (152), Expect = 2e-11
Identities = 21/21 (100%), Positives = 21/21 (100%)

```
Query: 1  SGSLSTFFRLFNRSFTQALGK 21
          SGSLSTFFRLFNRSFTQALGK
Sbjct: 26 SGSLSTFFRLFNRSFTQALGK 46
```

tr Q9APK7 **Competence stimulating protein [comC] [Streptococcus mutans]** 46 AA align

Score = 67.7 bits (152), Expect = 2e-11
Identities = 21/21 (100%), Positives = 21/21 (100%)

```
Query: 1  SGSLSTFFRLFNRSFTQALGK 21
          SGSLSTFFRLFNRSFTQALGK
Sbjct: 26 SGSLSTFFRLFNRSFTQALGK 46
```

tr Q9APK6 **Competence stimulating protein [comC] [Streptococcus mutans]** 43 AA align

Score = 56.6 bits (126), Expect = 4e-08
Identities = 17/18 (94%), Positives = 17/18 (94%)

```
Query: 1  SGSLSTFFRLFNRSFTQA 18
          SG LSTFFRLFNRSFTQA
Sbjct: 26 SGTLSTFFRLFNRSFTQA 43
```

tr Q7UJT6 **Acriflavine resistance protein B [acrB] [Rhodopirellula baltica]** 1072 AA align

Score = 31.6 bits (67), Expect = 1.4
Identities = 8/9 (88%), Positives = 8/9 (88%)

```
Query: 7   FFRLFNRSF 15
           FFRLFNR F
Sbjct: 540 FFRLFNRTF 548
```

sp P38771 FIL1_YEAST **FIL1 protein, mitochondrial precursor [FIL1] [Saccharomyces cerevisiae (Baker's yeast)]** 230 AA align

Score = 29.9 bits (63), Expect = 4.5
Identities = 8/9 (88%), Positives = 8/9 (88%)

```
Query: 9  RLFNRSFTQ 17
          RLFNRSF Q
Sbjct: 17 RLFNRSFSQ 25
```

tr Q7SAC2 **Predicted protein [NCU06309.1] [Neurospora crassa]** 699 AA align

Score = 29.9 bits (63), Expect = 4.5
Identities = 10/12 (83%), Positives = 10/12 (83%)

```
Query: 2   GSLSTFFRLFNR 13
           GS STF RLFNR
Sbjct: 422 GSPSTFMRLFNR 433
```

tr Q8EL34 **Hypothetical conserved protein [OB3397] [Oceanobacillus iheyensis]** 268 AA align

Score = 29.1 bits (61), Expect = 8.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

```
  Query: 3   SLSTFFRLF 11
             SLSTF+RLF
  Sbjct: 242 SLSTFYRLF 250



Database: EXPASY/UniProt
    Posted date:  Nov 8, 2004  3:52 PM
  Number of letters in database: 518,174,383
  Number of sequences in database:  1,621,919

Lambda     K      H
   0.348    0.289     1.75

Gapped
Lambda     K      H
   0.294    0.110    0.610


Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 21
length of database: 518,174,383
effective HSP length: 12
effective length of query: 9
effective length of database: 498,711,355
effective search space: 4488402195
effective search space used: 4488402195
T: 16
A: 40
X1: 14 ( 7.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 40 (21.9 bits)
S2: 61 (29.1 bits)
```

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NCBI PubMed National Library of Medicine NLM

Entrez PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Boo

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LinkOut
Cubby

Related Resources
Order Documents
NLM Catalog
NLM Gateway
TOXNET
Consumer Health
Clinical Alerts
ClinicalTrials.gov
PubMed Central

Display Summary Show: 20 Sort Send to

Items 1 - 11 of 11

1: Ooshima T, Osaka Y, Sasaki H, Osawa K, Yasuda H, Matsumoto M. Relate

Cariostatic activity of cacao mass extract.
Arch Oral Biol. 2000 Sep;45(9):805-8.
PMID: 10869494 [PubMed - indexed for MEDLINE]

2: Ooshima T, Osaka Y, Sasaki H, Osawa K, Yasuda H, Matsumura M, Sobue S, Matsumoto M. Relate

Caries inhibitory activity of cacao bean husk extract in in-vitro and animal e
Arch Oral Biol. 2000 Aug;45(8):639-45.
PMID: 10869475 [PubMed - indexed for MEDLINE]

3: Rose RK. Relate

Effects of an anticariogenic casein phosphopeptide on calcium diffusion in s model dental plaques.
Arch Oral Biol. 2000 Jul;45(7):569-75.
PMID: 10785520 [PubMed - indexed for MEDLINE]

4: Larsen MJ, Pearce EI, Ravnholt G. Relate

Dissolution of powdered human enamel suspended in acid solutions at a higl solid/solution ratio under a 5% CO2 atmosphere at 20 degrees C.
Arch Oral Biol. 1997 Sep;42(9):657-63.
PMID: 9403120 [PubMed - indexed for MEDLINE]

5: Tyler JE, Poole DF. Relate

Uptake of fluoride by human surface enamel from ammonium bifluoride anc reduction in the penetration in vitro by caries-like lesions.
Arch Oral Biol. 1984;29(12):971-4.
PMID: 6598366 [PubMed - indexed for MEDLINE]

6: Hayes ML. Relate

The inhibition of bacterial glycolysis in human dental plaque by medium-ch -sugar mouth-washes.
Arch Oral Biol. 1981;26(3):223-7. No abstract available.
PMID: 6947730 [PubMed - indexed for MEDLINE]

7: DePaola PF, Jordan HV, Soparkar PM. Relate

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Arch Oral Biol. 1977;22(3):187-91. No abstract available.
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